

X-15950.ST25.txt
SEQUENCE LISTING

<110> Applied Molecular Evolution, Inc.

<120> Human IL-1 Beta Antagonists

<130> X-15950

<150> 60/442,798

<151> 2003-01-24

<160> 68

<170> PatentIn version 3.2

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Lys Ala Ser Gln Asp Ile Asp Arg Phe Leu Ser
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 gtcactatca cttgcaaggc gagtcaggac attgataggt atttaagttg gttccagcag 180
 aaaccaggga aatctcctaa gaccctgac tctcgtgtaa agagattggg agatgggggtc 240
 ccatcaaggt tcagtggcag cgcattctgg caagattatt ctctcaccat cagcagcctg 300
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 caactcagca gcctgtcctc tgaggactct gccgtctatt attgttcaac aatctactat 360
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Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
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Gly Glu Ile Leu Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
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Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
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Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
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Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
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Gly Lys
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Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45

Tyr Arg Val Lys Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ile Gln Tyr Asp Glu Phe Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asp Arg Tyr
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Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys Phe
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X-15950.ST25.txt

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
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 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Asp Leu Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu

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335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
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Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
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Asp Arg Val Thr Ile Thr Cys Lys Phe Ser Gln Asp Ile Asp Arg Phe
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Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45

Tyr Arg Val Lys Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Asp Glu Phe Pro Tyr
 85 90 95

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Gly Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
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 Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Glu Ile Leu Pro Gly Ser Gly Thr Ile Asn Tyr Asn Glu Lys Phe
 50 55 60
 Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

X-15950.ST25.txt

Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Asp Asn Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365

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Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
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Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45

Tyr Arg Val Lys Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Asp Glu Phe Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu
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Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Asp Tyr Trp Gly Gln
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Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
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 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400

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Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 52
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 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Synthetic Construct

<400> 52

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Lys Phe Ser Gln Asp Ile Asp Arg Phe
 20 25 30

Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
 35 40 45

Tyr Arg Val Lys Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Asp Glu Phe Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

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Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu
 210

<210> 53
 <211> 450
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Synthetic Construct

<400> 53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asp Arg Tyr
 20 25 30

Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Asp Ile Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Ser Leu Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
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170

165

175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 225 230 235 240
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 245 250 255
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 260 265 270
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 275 280 285
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 290 295 300
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 305 310 315 320
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 325 330 335
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 340 345 350
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 355 360 365
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 370 375 380
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 385 390 395 400
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 405 410 415
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 420 425 430

X-15950.ST25.txt

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 435 440 445

Gly Lys
 450

<210> 54
 <211> 213
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Synthetic Construct

<400> 54

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asp Arg Phe
 20 25 30

Leu Ser Trp Phe Gln Gln Lys Pro Lys Ala Pro Lys Ser Leu Ile Tyr
 35 40 45

Arg Val Lys Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Asp Glu Phe Pro Tyr Thr
 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
 100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
 115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
 130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
 165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

195

200

X-15950.ST25.txt
205Asn Arg Gly Glu Cys
210<210> 55
<211> 407
<212> DNA
<213> HUMAN

<400> 55
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 tccgtgaagg tctcctgcaa ggcttctggc tacacattcg accgctattg gatcgagtgg 120
 gtgcgccagg cccctggcca aggcctggag tggatgggag agattctgcc tggcagcggc 180
 gacattaact acaatgagaa gttcaagggc cgcgtcacga ttaccgcgga caaatccacg 240
 agcacagcct acatggagct gagcagcctg cgctctgagg acacggccgt gtattactgt 300
 gcgcgcatgt actatgatta cgaccagggc tttgactact ggggccaggg caccctggtc 360
 accgtctcct ccgcctccac caagggccca tcggtcttcc cgctagc 407

<210> 56
<211> 407
<212> DNA
<213> HUMAN

<400> 56
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 gtgcgccagg cccctggcca aggcctggag tggatgggag agattctgcc tggcagcggc 180
 gacattaact acaatgagaa gttcaagggc cgcgtcacga ttaccgcgga caaatccacg 240
 agcacagcct acatggagct gagcagcctg cgctctgagg acacggccgt gtattactgt 300
 gcgcgcatgt actatgatta cgaccagggc tttgacctgt ggggccaggg caccctggtc 360
 accgtctcct ccgcctccac caagggccca tcggtcttcc cgctagc 407

<210> 57
<211> 407
<212> DNA
<213> HUMAN

<400> 57
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 tccgtgaagg tctcctgcaa ggcttctggc tacacattcg accgctattg gatcgagtgg 120
 gtgcgccagg cccctggcca aggcctggag tggatgggag agattctgcc tggcagcggc 180
 accattaact acaatgagaa gttcaagggc cgcgtcacga ttaccgcgga caaatccacg 240
 agcacagcct acatggagct gagcagcctg cgctctgagg acacggccgt gtattactgt 300
 gcgcgcatgt actatgatta cgaccagggc tttgacaact ggggccaggg caccctggtc 360

X-15950.ST25.txt

accgtctcct ccgcctccac caagggccca tcggtcttcc cgctagc 407

<210> 58
<211> 407
<212> DNA
<213> HUMAN

<400> 58
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gtgcgccagg cccctggcca aggcctggag tggatgggag agattctgcc tggcagcggc 180
gacattaact acaatgagaa gttcaagggc cgcgtcacga ttaccgcgga caaatccacg 240
agcacagcct acatggagct gagcagcctg cgctctgagg acacggccgt gtattactgt 300
gcgcgcatgt actatgatta cgaccagggc tttagcctgt ggggccaggg caccctgggtc 360
accgtctcct ccgcctccac caagggccca tcggtcttcc cgctagc 407

<210> 59
<211> 407
<212> DNA
<213> HUMAN

<400> 59
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tccgtgaagg tctcctgcaa ggcttctggc tacacattcg accgctattg gatcgagtgg 120
gtgcgccagg cccctggcca aggcctggag tggatgggag agattctgcc tggcagcggc 180
gacattaact acaatgagaa gttcaagggc cgcgtcacga ttaccgcgga caaatccacg 240
agcacagcct acatggagct gagcagcctg cgctctgagg acacggccgt gtattactgt 300
gcgcgcatgt actatgatta cgaccagggc tttgactact ggggccaggg caccctgggtc 360
accgtctcct ccgcctccac caagggccca tcggtcttcc cgctagc 407

<210> 60
<211> 321
<212> DNA
<213> HUMAN

<400> 60
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ggcaaagccc ctaagtcctt gatctatcgc gtgaagcgcc tggatggatgg cgtcccatcc 180
cgcttcagcg gcagtggctc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgcatccag tatgatgagt ttccgtacac cttcggcggc 300
ggcaccaagg tggagatcaa a 321

<210> 61
<211> 321
<212> DNA

X-15950.ST25.txt

<213> HUMAN

<400> 61

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ggcaaagccc ctaagtcctt gatctatcgc gtgaagcgcc tggatggatgg cgtcccatcc 180
cgcttcagcg gcagtggctc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgcgttcag tatgatgagt ttccgtacgg ttccggcggc 300
ggcaccaagg tggagatcaa a 321

<210> 62

<211> 321

<212> DNA

<213> HUMAN

<400> 62

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atcacttgta agttcagtca ggacattgat cgcttcctga gctgggtttca gcagaaacca 120
ggcaaagccc ctaagtcctt gatctatcgc gtgaagcgcc tggatggatgg cgtcccatcc 180
cgcttcagcg gcagtggctc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgcgttcag tatgatgagt ttccgtacac cttcggcggc 300
ggcaccaagg tggagatcaa a 321

<210> 63

<211> 321

<212> DNA

<213> HUMAN

<400> 63

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atcacttgta agttcagtca ggacattgat cgcttcctga gctgggtttca gcagaaacca 120
ggcaaagccc ctaagtcctt gatctatcgc gtgaagcgcc tggatggatgg cgtcccatcc 180
cgcttcagcg gcagtggctc tggcacagat ttactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgcgttcag tatgatgagt ttccgtacac cttcggcggc 300
ggcaccaagg tggagatcaa a 321

<210> 64

<211> 321

<212> DNA

<213> HUMAN

<400> 64

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atcacttgta aggcgagtca ggacattgat cgcttcctga gctgggtttca gcagaaacca 120
ggcaaagccc ctaagtcctt gatctatcgc gtgaagcgcc tggatggatgg cgtcccatcc 180
cgcttcagcg gcagtggctc tggcacagat ttactctca ccatcagcag cctgcagcct 240

X-15950.ST25.txt

gaagattttg caacttatta ctgctgttcag tatgatgagt ttccgtacac cttcggcggc 300
ggcaccagg tggagatcaa a 321

<210> 65
<211> 990
<212> DNA
<213> HUMAN

<400> 65
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aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 180
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac 240
atctgcaacg tgaatcaca gccccagcaac accaagggtg acaagaaagt tgagcccaaa 300
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg 360
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccttgag 420
gtcacatgcg tgggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac 480
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 540
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 600
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gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggacgagctg 720
accaagaacc aggtcagcct gacctgctg gtcaaaggct tctatcccag cgacatcgcc 780
gtggagtggg agagcaatgg gcagccggag acaactaca agaccacgcc ccccggtgctg 840
gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag 900
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 960
aagagcctct ccctgtctcc gggtaaatga 990

<210> 66
<211> 952
<212> DNA
<213> HUMAN

<400> 66
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gactacttcc ccgaaccggt gacggtgtcg tggaaactcag gcgccctgac cagcggcgtg 120
cacaccttcc cggctgtcct acagtctca ggactctact ccctcagcag cgtggtgacc 180
gtgccctcca gcagcttggg cacgaagacc tacacctgca acgtagatca caagcccagc 240
aacaccaagg tggacaagag agttgagtcc aaatatggtc ccccatgccc accctgcccc 300
gcacctgagt tcctgggggg accatcagtc ttctgttcc ccccaaaacc caaggacact 360
ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 420

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cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 480
ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 540
caggactggc tgaacggcaa ggagtacaag tgcaagggtct ccaacaaagg cctcccgtcc 600
tccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 660
ctgcccccat cccaggagga gatgaccaag aaccagggtca gcctgacctg cctgggtcaaa 720
ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 780
tacaagacca cgctcccgt gctggactcc gacggctcct tcttctcta cagcaggcta 840
accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 900
gctctgcaca accactacac acagaagagc ctctccctgt ctctgggtaa at 952

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<210> 67
 <211> 324
 <212> DNA
 <213> HUMAN

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<400> 67
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ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120
tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180
agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240
aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcaciaag 300
agcttcaaca ggggagagtg ctaa 324

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<210> 68
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 68

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
20 25 30

Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr
35 40 45

Phe Asp Arg Tyr Trp Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly
50 55 60

Leu Glu Trp Met Gly Glu Ile Leu Pro Gly Ser Gly Asp Ile Asn Tyr
65 70 75 80

X-15950.ST25.txt

Asn Glu Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr
 85 90 95
 Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
 100 105 110
 Val Tyr Tyr Cys Ala Arg Met Tyr Tyr Asp Tyr Asp Gln Gly Phe Asp
 115 120 125
 Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 130 135 140
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 145 150 155 160
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn
 210 215 220
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser
 225 230 235 240
 Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly
 245 250 255
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 260 265 270
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
 275 280 285
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 290 295 300
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
 305 310 315 320
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 325 330 335
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
 340 345 350

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Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
405 410 415

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
420 425 430

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
435 440 445

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
450 455 460

Leu Gly Lys
465